



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/980,839

DATE: 07/25/2002

TIME: 11:40:45

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3 <110> APPLICANT: FLAMAND, MARIE
 4 MEGRET, FRANCOIS
 5 ALCON, SOPHIE
 6 TALARMIN, ANTOINE
 7 DESPRES, PHILIPPE
 8 DEUBEL, VINCENT
 10 <120> TITLE OF INVENTION: EARLY DETECTION OF FLAVIVIRUSES USING THE NS1
 11 GLYCOPROTEIN
 13 <130> FILE REFERENCE: 03495-0213
 15 <140> CURRENT APPLICATION NUMBER: 09/980,839
 C--> 16 <141> CURRENT FILING DATE: 2002-06-21
 18 <150> PRIOR APPLICATION NUMBER: PCT/FR00/01620
 19 <151> PRIOR FILING DATE: 2000-06-09
 21 <150> PRIOR APPLICATION NUMBER: FR 99/07290
 22 <151> PRIOR FILING DATE: 1999-06-09
 24 <150> PRIOR APPLICATION NUMBER: FR 99/07361
 25 <151> PRIOR FILING DATE: 1999-06-10
 27 <160> NUMBER OF SEQ ID NOS: 2
 29 <170> SOFTWARE: PatentIn Ver. 2.1
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 1137
 33 <212> TYPE: DNA
 34 <213> ORGANISM: Dengue virus type 1
 36 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 38 <222> LOCATION: (1)..(1134)
 40 <400> SEQUENCE: 1
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 42 Met Arg Ser Ala Ser Leu Ser Met Thr Cys Ile Ala Val Gly Met Val
 43 1 5 10 15
 45 aca ctg tac cta gga gtc atg gtt caa gcg gac tcg gga tgt gta atc 96
 46 Thr Leu Tyr Leu Gly Val Met Val Gln Ala Asp Ser Gly Cys Val Ile
 47 20 25 30
 49 aac tgg aag ggc aga gaa ctc aaa tgt gga agt ggc att ttt gtc act 144
 50 Asn Trp Lys Gly Arg Glu Leu Lys Cys Gly Ser Gly Ile Phe Val Thr
 51 35 40 45
 53 aat gaa gtc cac act tgg aca gag caa tac aaa ttc cag gct gac tcc 192
 54 Asn Glu Val His Thr Trp Thr Glu Gln Tyr Lys Phe Gln Ala Asp Ser
 55 50 55 60
 57 cca aaa aga ctg tca gca gcc att ggg aag gca tgg gag gag ggc gtg 240
 58 Pro Lys Arg Leu Ser Ala Ala Ile Gly Lys Ala Trp Glu Glu Gly Val
 59 65 70 75 80
 61 tgt gga att cga tca gcc acg cgt ctt gag aac atc atg tgg aag caa 288

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62	Cys	Gly	Ile	Arg	Ser	Ala	Thr	Arg	Leu	Glu	Asn	Ile	Met	Trp	Lys	Gln	
63					85					90					95		
65	ata	tca	aat	gaa	ttg	aac	cac	att	cta	ctt	gaa	aat	gac	atg	aaa	ttc	336
66	Ile	Ser	Asn	Glu	Leu	Asn	His	Ile	Leu	Leu	Glu	Asn	Asp	Met	Lys	Phe	
67				100					105					110			
69	aca	gtg	gtt	gta	gga	gat	gct	aat	gga	att	ttg	gcc	cag	ggg	aaa	aaa	384
70	Thr	Val	Val	Val	Gly	Asp	Ala	Asn	Gly	Ile	Leu	Ala	Gln	Gly	Lys	Lys	
71			115					120					125				
73	atg	atc	agg	cca	caa	ccc	atg	gaa	cac	aaa	tac	tca	tgg	aaa	agc	tgg	432
74	Met	Ile	Arg	Pro	Gln	Pro	Met	Glu	His	Lys	Tyr	Ser	Trp	Lys	Ser	Trp	
75		130					135					140					
77	gga	aaa	gcc	aag	atc	ata	gga	gca	gac	aca	cag	aat	acc	acc	ttc	atc	480
78	Gly	Lys	Ala	Lys	Ile	Ile	Gly	Ala	Asp	Thr	Gln	Asn	Thr	Thr	Phe	Ile	
79	145					150					155					160	
81	atc	gac	ggc	cca	gac	act	cca	gaa	tgc	ccc	gat	gac	caa	aga	gcg	tgg	528
82	Ile	Asp	Gly	Pro	Asp	Thr	Pro	Glu	Cys	Pro	Asp	Asp	Gln	Arg	Ala	Trp	
83				165					170					175			
85	aac	att	tgg	gaa	gtt	gag	gac	tat	ggg	ttt	gga	att	ttc	acg	aca	aac	576
86	Asn	Ile	Trp	Glu	Val	Glu	Asp	Tyr	Gly	Phe	Gly	Ile	Phe	Thr	Thr	Asn	
87			180						185				190				
89	ata	tgg	ctg	aaa	ttg	cgt	gac	tcc	tac	acc	caa	atg	tgt	gac	cac	cgg	624
90	Ile	Trp	Leu	Lys	Leu	Arg	Asp	Ser	Tyr	Thr	Gln	Met	Cys	Asp	His	Arg	
91			195					200					205				
93	cta	atg	tca	gct	gcc	gtc	aag	gac	agc	aag	gca	gtc	cat	gct	gac	atg	672
94	Leu	Met	Ser	Ala	Ala	Val	Lys	Asp	Ser	Lys	Ala	Val	His	Ala	Asp	Met	
95		210				215					220						
97	ggg	tac	tgg	ata	gaa	agt	gaa	aag	aac	gag	acc	tgg	aag	cta	gcg	aga	720
98	Gly	Tyr	Trp	Ile	Glu	Ser	Glu	Lys	Asn	Glu	Thr	Trp	Lys	Leu	Ala	Arg	
99	225				230				235				240				
101	gcc	tcc	ttc	ata	gaa	gtc	aag	aca	tgc	att	tgg	ccg	aaa	tcc	cac	act	768
102	Ala	Ser	Phe	Ile	Glu	Val	Lys	Thr	Cys	Ile	Trp	Pro	Lys	Ser	His	Thr	
103				245					250				255				
105	cta	tgg	agt	aat	gga	gtt	ttg	gaa	agt	gaa	atg	ata	atc	cca	aag	ata	816
106	Leu	Trp	Ser	Asn	Gly	Val	Leu	Glu	Ser	Glu	Met	Ile	Ile	Pro	Lys	Ile	
107				260				265					270				
109	tat	gga	gga	cca	ata	tct	cag	cac	aat	tac	aga	cca	ggg	tat	ttc	aca	864
110	Tyr	Gly	Gly	Pro	Ile	Ser	Gln	His	Asn	Tyr	Arg	Pro	Gly	Tyr	Phe	Thr	
111			275				280					285					
113	caa	aca	gca	ggg	cca	tgg	cac	cta	ggt	aag	ttg	gaa	ttg	gat	ttt	gac	912
114	Gln	Thr	Ala	Gly	Pro	Trp	His	Leu	Gly	Lys	Leu	Glu	Leu	Asp	Phe	Asp	
115		290				295					300						
117	ttg	tgt	gaa	ggc	acc	aca	gtt	gtt	gtg	gat	gaa	cat	tgt	gga	aat	cga	960
118	Leu	Cys	Glu	Gly	Thr	Thr	Val	Val	Val	Asp	Glu	His	Cys	Gly	Asn	Arg	
119	305				310				315				320				
121	ggt	cca	tct	ctc	aga	act	aca	aca	gtc	aca	gga	aag	ata	atc	cat	gaa	1008
122	Gly	Pro	Ser	Leu	Arg	Thr	Thr	Thr	Val	Thr	Gly	Lys	Ile	Ile	His	Glu	
123				325					330				335				
125	tgg	tgt	tgc	aga	tcc	tgc	acg	tta	ccc	ccc	tta	cgc	ttc	aga	gga	gaa	1056
126	Trp	Cys	Cys	Arg	Ser	Cys	Thr	Leu	Pro	Pro	Leu	Arg	Phe	Arg	Gly	Glu	

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127          340          345          350
129 gac gga tgt tgg tat ggc atg gaa atc aga cca gtt aag gag aag gag 1104
130 Asp Gly Cys Trp Tyr Gly Met Glu Ile Arg Pro Val Lys Glu Lys Glu
131          355          360          365
133 gag aac cta gtt agg tca atg gtc tct gca taa 1137
134 Glu Asn Leu Val Arg Ser Met Val Ser Ala
135          370          375
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 378
140 <212> TYPE: PRT
141 <213> ORGANISM: Dengue virus type 1
143 <400> SEQUENCE: 2
144 Met Arg Ser Ala Ser Leu Ser Met Thr Cys Ile Ala Val Gly Met Val
145 1 5 10 15
147 Thr Leu Tyr Leu Gly Val Met Val Gln Ala Asp Ser Gly Cys Val Ile
148 20 25 30
150 Asn Trp Lys Gly Arg Glu Leu Lys Cys Gly Ser Gly Ile Phe Val Thr
151 35 40 45
153 Asn Glu Val His Thr Trp Thr Glu Gln Tyr Lys Phe Gln Ala Asp Ser
154 50 55 60
156 Pro Lys Arg Leu Ser Ala Ile Gly Lys Ala Trp Glu Glu Gly Val
157 65 70 75 80
159 Cys Gly Ile Arg Ser Ala Thr Arg Leu Glu Asn Ile Met Trp Lys Gln
160 85 90 95
162 Ile Ser Asn Glu Leu Asn His Ile Leu Glu Asn Asp Met Lys Phe
163 100 105 110
165 Thr Val Val Val Gly Asp Ala Asn Gly Ile Leu Ala Gln Gly Lys Lys
166 115 120 125
168 Met Ile Arg Pro Gln Pro Met Glu His Lys Tyr Ser Trp Lys Ser Trp
169 130 135 140
171 Gly Lys Ala Lys Ile Ile Gly Ala Asp Thr Gln Asn Thr Thr Phe Ile
172 145 150 155 160
174 Ile Asp Gly Pro Asp Thr Pro Glu Cys Pro Asp Asp Gln Arg Ala Trp
175 165 170 175
177 Asn Ile Trp Glu Val Glu Asp Tyr Gly Phe Gly Ile Phe Thr Thr Asn
178 180 185 190
180 Ile Trp Leu Lys Leu Arg Asp Ser Tyr Thr Gln Met Cys Asp His Arg
181 195 200 205
183 Leu Met Ser Ala Ala Val Lys Asp Ser Lys Ala Val His Ala Asp Met
184 210 215 220
186 Gly Tyr Trp Ile Glu Ser Glu Lys Asn Glu Thr Trp Lys Leu Ala Arg
187 225 230 235 240
189 Ala Ser Phe Ile Glu Val Lys Thr Cys Ile Trp Pro Lys Ser His Thr
190 245 250 255
192 Leu Trp Ser Asn Gly Val Leu Glu Ser Glu Met Ile Ile Pro Lys Ile
193 260 265 270
195 Tyr Gly Gly Pro Ile Ser Gln His Asn Tyr Arg Pro Gly Tyr Phe Thr
196 275 280 285
198 Gln Thr Ala Gly Pro Trp His Leu Gly Lys Leu Glu Leu Asp Phe Asp

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199	290	295	300
201 Leu Cys Glu Gly Thr Thr Val Val Val Asp Glu His Cys Gly Asn Arg			
202 305	310	315	320
204 Gly Pro Ser Leu Arg Thr Thr Thr Val Thr Gly Lys Ile Ile His Glu			
205	325	330	335
207 Trp Cys Cys Arg Ser Cys Thr Leu Pro Pro Leu Arg Phe Arg Gly Glu			
208	340	345	350
210 Asp Gly Cys Trp Tyr Gly Met Glu Ile Arg Pro Val Lys Glu Lys Glu			
211	355	360	365
213 Glu Asn Leu Val Arg Ser Met Val Ser Ala			
214	370	375	

VERIFICATION SUMMARY

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date